# RAW SEQUENCE LISTING
## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/764,818_

Source: _1FWO_

Date Processed by STIC: _2/9/04_

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
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_Effective 12/13/03_: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

IFWO

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   3 <110> APPLICANT: ADViSYS
   5 <120> TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE ("GHRH") TREATMENT
DECREASES CULLING IN
   6        HERD ANIMALS
   8 <130> FILE REFERENCE: 108328.00170 - AVSI-0033
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/764,818
C--> 10 <141> CURRENT FILING DATE: 2004-01-26
  10 <160> NUMBER OF SEQ ID NOS: 30
  12 <170> SOFTWARE: PatentIn version 3.1
  14 <210> SEQ ID NO: 1
  15 <211> LENGTH: 40
  16 <212> TYPE: PRT
  17 <213> ORGANISM: artificial sequence
  19 <220> FEATURE:
  20 <223> OTHER INFORMATION: This is the amino acid sequenc for HV-GHRH.
  22 <400> SEQUENCE: 1
  24 His Val Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Ala Gln
  25 1               5                   10                  15
  28 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Leu Asn Arg Gln Gln Gly
  29              20                  25                  30
  32 Glu Arg Asn Gln Glu Gln Gly Ala
  33          35                  40
  36 <210> SEQ ID NO: 2
  37 <211> LENGTH: 40
  38 <212> TYPE: PRT
  39 <213> ORGANISM: artificial sequence
  41 <220> FEATURE:
  42 <223> OTHER INFORMATION: This is the amino acid sequenc for TI-GHRH.
  44 <400> SEQUENCE: 2
  46 Tyr Ile Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Ala Gln
  47 1               5                   10                  15
  50 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Leu Asn Arg Gln Gln Gly
  51              20                  25                  30
  54 Glu Arg Asn Gln Glu Gln Gly Ala
  55          35                  40
  58 <210> SEQ ID NO: 3
  59 <211> LENGTH: 40
  60 <212> TYPE: PRT
  61 <213> ORGANISM: artificial sequence
  63 <220> FEATURE:
  64 <223> OTHER INFORMATION: This is the amino acid sequenc for TV-GHRH.
  66 <400> SEQUENCE: 3
  68 Tyr Val Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Ala Gln
  69 1               5                   10                  15
```

*Does Not Comply*
*Corrected Diskette Needed*

*p. 3*

```
72 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Leu Asn Arg Gln Gln Gly
73           20                  25                  30
76 Glu Arg Asn Gln Glu Gln Gly Ala
77           35                  40
80 <210> SEQ ID NO: 4
81 <211> LENGTH: 40
82 <212> TYPE: PRT
83 <213> ORGANISM: artificial sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: This is the amino acid sequenc for 15/27/28-GHRH.
88 <400> SEQUENCE: 4
90 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Ala Gln
91 1            5                  10                  15
94 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Leu Asn Arg Gln Gln Gly
95           20                  25                  30
98 Glu Arg Asn Gln Glu Gln Gly Ala
99           35                  40
102 <210> SEQ ID NO: 5
103 <211> LENGTH: 44
104 <212> TYPE: PRT
105 <213> ORGANISM: artificial sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: This is a consensus sequence for GHRH
110 <400> SEQUENCE: 5
112 Thr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
113 1            5                  10                  15
116 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
117           20                  25                  30
120 Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
121           35                  40
124 <210> SEQ ID NO: 6
125 <211> LENGTH: 40
126 <212> TYPE: PRT
127 <213> ORGANISM: artificial sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: This is the artificial sequence for GHRH (1-40)OH.
132 <220> FEATURE:
133 <221> NAME/KEY: MISC_FEATURE
134 <222> LOCATION: (1)..(1)
135 <223> OTHER INFORMATION: Xaa at position 1 may be tyrosine, or histidine
138 <220> FEATURE:
139 <221> NAME/KEY: MISC_FEATURE
140 <222> LOCATION: (2)..(2)
141 <223> OTHER INFORMATION: Xaa at position 2 may be alanine, valine, or isoleucine.
144 <220> FEATURE:
145 <221> NAME/KEY: MISC_FEATURE
146 <222> LOCATION: (15)..(15)
147 <223> OTHER INFORMATION: Xaa at position 15 may be alanine, valine, or isoleucine.
150 <220> FEATURE:
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            RAW SEQUENCE LISTING                    DATE: 02/09/2004
            PATENT APPLICATION: US/10/764,818       TIME: 10:36:04

            Input Set : N:\FATIMA\10764818.txt
            Output Set: N:\CRF4\02062004\J764818.raw
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151 <221> NAME/KEY: MISC_FEATURE
152 <222> LOCATION: (27)..(27)
153 <223> OTHER INFORMATION: Xaa at position 27 may be methionine, or leucine.
156 <220> FEATURE:
157 <221> NAME/KEY: MISC_FEATURE
158 <222> LOCATION: (28)..(28)
159 <223> OTHER INFORMATION: Xaa at position 28 may be serine or asparagine.
162 <220> FEATURE:
163 <221> NAME/KEY: MISC_FEATURE
164 <222> LOCATION: (34)..(34)
165 <223> OTHER INFORMATION: ARG may also be SER
168 <220> FEATURE:
169 <221> NAME/KEY: MISC_FEATURE
170 <222> LOCATION: (38)..(38)
171 <223> OTHER INFORMATION: Gln may also be Arg
174 <400> SEQUENCE: 6
176 Xaa Xaa Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Xaa Gln
177 1               5                   10                  15
180 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Xaa Xaa Arg Gln Gln Gly
181             20                  25                  30
184 Glu Arg Asn Gln Glu Gln Gly Ala
185         35                  40
188 <210> SEQ ID NO: 7
189 <211> LENGTH: 323
190 <212> TYPE: DNA
191 <213> ORGANISM: artificial sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: This is a nucleic acid sequence of a eukaryotic promoter c5-
12.
196 <400> SEQUENCE: 7
197 cggccgtccg ccctcggcac catcctcacg acacccaaat atggcgacgg gtgaggaatg     60
199 gtgggggagtt attttagag cggtgaggaa ggtgggcagg cagcaggtgt tggcgctcta    120
201 aaaataactc ccgggagtta tttttagagc ggaggaatgg tggacaccca aatatggcga   180
203 cggttcctca cccgtcgcca tatttgggtg tccgccctcg gccggggccg cattcctggg   240
205 ggccgggcgg tgctcccgcc cgcctcgata aaaggctccg gggccggcgg cggcccacga   300
207 gctacccgga ggagcgggag gcg                                            323
210 <210> SEQ ID NO: 9
211 <211> LENGTH: 190
212 <212> TYPE: DNA
213 <213> ORGANISM: artificial sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Nucleic acid sequence of a hGH poly A tail.
218 <400> SEQUENCE: 8
219 gggtggcatc cctgtgaccc ctcccagtg cctctcctgg ccctggaagt tgccactcca     60
221 gtgcccacca gccttgtcct aataaaatta agttgcatca ttttgtctga ctaggtgtcc   120
223 ttctataata ttatggggtg gaggggggtg gtatggagca aggggcaagt tgggaagaca   180
225 acctgtaggg                                                          190
228 <210> SEQ ID NO: 9
229 <211> LENGTH: 219
230 <212> TYPE: DNA
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W--> (handwritten note at line 176)

Handwritten annotations:
"Arg can only represent itself, nothing else. Use "Xaa", instead, and explain in <2207>-<2237> section"
"Same error — use Xaa and explain"

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                    RAW SEQUENCE LISTING          DATE: 02/09/2004
                    PATENT APPLICATION:  US/10/764,818     TIME: 10:36:04

                    Input Set : N:\FATIMA\10764818.txt
                    Output Set: N:\CRF4\02062004\J764818.raw
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231 <213> ORGANISM: artificial sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: This is the cDNA for Porcine GHRH.
236 <400> SEQUENCE: 9
237 atggtgctct gggtgttctt ctttgtgatc ctcaccctca gcaacagctc ccactgctcc      60
239 ccactccccc ctttgacctt caggatgcgg cggcacgtag atgccatctt caccaacagc     120
241 taccggaagg tgctggccca gctgtccgcc cgcaagctgc tccaggacat cctgaacagg     180
243 cagcagggag agaggaacca agagcaagga gcataatga                           219
246 <210> SEQ ID NO: 10
247 <211> LENGTH: 40
248 <212> TYPE: PRT
249 <213> ORGANISM: artificial sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: This is the amino acid sequence for porcine GHRH.
254 <400> SEQUENCE: 10
256 Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
257 1               5                   10                  15
260 Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
261             20                  25                  30
264 Glu Arg Asn Gln Glu Gln Gly Ala
265             35                  40
268 <210> SEQ ID NO: 11
269 <211> LENGTH: 3534
270 <212> TYPE: DNA
271 <213> ORGANISM: artificial sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: This is the nucleic acid sequence for the operatively linked
comp
275         onents of the HV-GHRH plasmid.
277 <400> SEQUENCE: 11
278 gttgtaaaac gacggccagt gaattgtaat acgactcact ataggcgaa ttggagctcc      60
280 accgcggtgg cggccgtccg ccctcggcac catcctcacg acacccaaat atggcgacgg     120
282 gtgaggaatg gtggggagtt attttagag cggtgaggaa ggtgggcagg cagcaggtgt     180
284 tggcgctcta aaaataactc ccgggagtta tttttagagc ggaggaatgg tggacaccca     240
286 aatatggcga cgggtcctca cccgtcgcca tatttgggtg tccgccctcg gccggggccg     300
288 cattcctggg ggccgggcgg tgctcccgcc cgcctcgata aaaggctccg gggccggccgg    360
290 cggcccacga gctacccgga ggagcgggag gcgccaagct ctagaactag tggatcccaa     420
292 ggcccaactc cccgaaccac tcagggtcct gtggacagct cacctagctg ccatggtgct     480
294 ctgggtgttc ttctttgtga tcctcaccct cagcaacagc tcccactgct cccaccctcc     540
296 ccctttgacc ctcaggatgc ggcggcacgt agatgccatc ttcaccaaca gctaccggaa     600
298 ggtgctggcc cagctgtccg cccgcaagct gctccaggac atcctgaaca ggcagcaggg     660
300 agagaggaac caagagcaag gagcataatg actgcaggaa ttcgatatca agcttatcgg     720
302 ggtggcatcc ctgtgacccc tcccagtgc ctctcctggc cctggaagtt gccactccag     780
304 tgcccaccag ccttgtccta ataaaattaa gttgcatcat tttgtctgac taggtgtcct     840
306 tctataatat tatggggtgg aggggggtgg tatggagcaa ggggcaagtt gggaagacaa     900
308 cctgtaggcg ctgcggggtc tattgggaac caagctggag tgcagtggca caatcttggc     960
310 tcactgcaat ctccgcctcc tgggttcaag cgattctcct gcctcagcct cccgagttgt    1020
312 tgggattcca ggcatgcatg accaggctca gctaatttt gttttttggg tagagacggg     1080
314 gtttcaccat attggccagg ctggtctcca actcctaatc tcaggtgatc tacccacctt    1140
316 ggcctcccaa attgctggga ttacaggcgt gaaccactgc tcccttcct gtccttctga    1200
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318 ttttaaaata actataccag caggaggacg tccagacaca gcataggcta cctggccatg   1260
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322 ctcagtagat gcctgttgaa ttcgataccg tcgacctcga gggggggccc ggtaccagct   1380
324 tttgttccct ttagtgaggg ttaatttcga gcttggcgta atcatggtca tagctgtttc   1440
326 ctgtgtgaaa ttgttatccg ctcacaattc cacacaacat acgagccgga agcataaagt   1500
328 gtaaagcctg gggtgcctaa tgagtgagct aactcacatt aattgcgttg cgctcactgc   1560
330 ccgctttcca gtcgggaaac ctgtcgtgcc agctgcatta atgaatcggc caacgcgcgg   1620
332 ggagagggcg tttgcgtatt gggcgctctt ccgcttcctc gctcactgac tcgctgcgct   1680
334 cggtcgttcg gctgcggcga gcggtatcag ctcactcaaa ggcggtaata cggttatcca   1740
336 cagaatcagg ggataacgca ggaaagaaca tgtgagcaaa aggccagcaa aaggccagga   1800
338 accgtaaaaa ggccgcgttg gtggcgtttt tccataggct ccgcccccct gacgagcatc   1860
340 acaaaaatcg acgctcaagt cagaggtggc gaaacccgac aggactataa agataccagg   1920
342 cgtttccccc tggaagctcc ctcgtgcgct ctcctgttcc gaccctgccg cttaccggat   1980
344 acctgtccgc ctttctcct tcgggaagcg tggcgctttc tcatagctca cgctgtaggt   2040
346 atctcagttc ggtgtaggtc gttcgctcca agctgggctg tgtgcacgaa cccccccgttc   2100
348 agcccgaccg ctgcgcctta tccggtaact atcgtcttga gtccaacccg gtaagacacg   2160
350 acttatcgcc actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg   2220
352 gtgctacaga gttcttgaag tggtggccta actacggcta cactagaaga acagtatttg   2280
354 gtatctgcgc tctgctgaag ccagttacct tcggaaaaag agttggtagc tcttgatccg   2340
356 gcaaacaaac caccgctggt agcggtggtt tttttgtttg caagcagcag attacgcgca   2400
358 gaaaaaaagg atctcaagaa gatcctttga tcttttctac ggggtctgac gctcagaaga   2460
360 actcgtcaag aaggcgatag aaggcgatgc gctgcgaatc gggagcggcg ataccgtaaa   2520
362 gcacgaggaa gcggtcagcc cattcgccgc caagctcttc agcaatatca cgggtagcca   2580
364 acgctatgtc tgatagcgg tccgccacac ccagccgcc acagtcgatg aatccagaaa   2640
366 agcggccatt ttccaccatg atattcggca agcaggcatc gccatgggtc acgacgagat   2700
368 cctccgcgtc gggcatgcgc gccttgagcc tggcgaacag ttcggctggc gcgagcccct   2760
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372 gctcgatgcg atgtttcgct tggtggtcga atgggcaggt agccggatca agcgtatgca   2880
374 gccgccgcat tgcatcagcc atgatggata cttttctcggc aggacaagg tgagatgaca   2940
376 ggagatcctg ccccggcact tcgcccaata gcagccagtc ccttcccgct tcagtgacaa   3000
378 cgtcgagcac agctgcgcaa ggaacgcccg tcgtggccag ccacgatagc cgcgctgcct   3060
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382 cctgcgctga cagccggaac acggcggcat cagagcagcc gattgtctgt tgtgcccagt   3180
384 catagccgaa tagcctctcc acccaagcgg ccggagaacc tgcgtgcaat ccatcttgtt   3240
386 caatcatgcg aaacgatcct catctgtct cttgatcaga tcttgatcc ctgcgccatc   3300
388 agatccttgg cggcaagaaa gccatccagt ttacttttgca gggcttccca accttaccag   3360
390 agggcgcccc agctggcaat tccggttcgc ttgctgtcca taaaaccgcc cagtctagca   3420
392 actgttggga agggcgatcg gtgcgggcct cttcgctatt acgccagctg gcgaaagggg   3480
394 gatgtgctgc aaggcgatta agttgggtaa cgccaggggtt ttcccagtca cgac         3534
397 <210> SEQ ID NO: 12
398 <211> LENGTH: 3534
399 <212> TYPE: DNA
400 <213> ORGANISM: artificial sequence
402 <220> FEATURE:
403 <223> OTHER INFORMATION: Nucleic acid sequence for the TI-GHRH plasmid.
405 <400> SEQUENCE: 12
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408 accgcggtgg cggccgtccg ccctcggcac catcctcacg acacccaaat atggcgacgg      120
410 gtgaggaatg gtgggggagtt atttttagag cggtgaggaa ggtgggcagg cagcaggtgt     180
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/09/2004
PATENT APPLICATION: US/10/764,818 TIME: 10:36:05

Input Set : N:\FATIMA\10764818.txt
Output Set: N:\CRF4\02062004\J764818.raw

**Please Note:**
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:6; Xaa Pos. 1,2,15,27,28

**Invalid Line Length:**
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

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                    VERIFICATION SUMMARY              DATE: 02/09/2004
                    PATENT APPLICATION:  US/10/764,818    TIME: 10:36:05

                    Input Set : N:\FATIMA\10764818.txt
                    Output Set: N:\CRF4\02062004\J764818.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
M:341 Repeated in SeqNo=6
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